

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/052,545DATE: 02/13/2002
TIME: 21:09:06

INPUT SET: S36758.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT:

(A) NAME: Jarl Wikberg
(B) STREET: Trillvaegen 13
(C) CITY: Umea
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP): 905 92 Umea

(A) NAME: Vijay Chhajlani
(B) STREET: Stigbergsvaegen
(C) CITY: Uppsala
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP): 752 42 Uppsala

(ii) TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
(B) STREET: 1100 New York Ave., N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/052,545
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/387,805
(B) FILING DATE: 21-FEB-95

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/052,545DATE: 02-13-2002
TIME: 21:09:06

INPUT SET: S36758.raw

47 (A) APPLICATION NUMBER: PCT/DK93/00273
48 (B) FILING DATE: 20-AUG-93
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: DK 1046/92
52 (B) FILING DATE: 21-AUG-92
53
54 (vii) PRIOR APPLICATION DATA:
55 (A) APPLICATION NUMBER: DK 1118/92
56 (B) FILING DATE: 10-SEP-92
57
58 (vii) PRIOR APPLICATION DATA:
59 (A) APPLICATION NUMBER: DK 0528/93
60 (B) FILING DATE: 05-MAY-93
61
62 (viii) ATTORNEY/AGENT INFORMATION:
63 (A) NAME: Cimbala, Michele A.
64 (B) REGISTRATION NUMBER: 33,851
65 (C) REFERENCE/DOCKET NUMBER: 1102.0160000
66
67 (ix) TELECOMMUNICATION INFORMATION:
68 (A) TELEPHONE: (202)371-2600
69 (B) TELEFAX: (202) 371-2540
70
71 (2) INFORMATION FOR SEQ ID NO: 1:
72
73 (i) SEQUENCE CHARACTERISTICS:
74 (A) LENGTH: 1270 base pairs
75 (B) TYPE: nucleic acid
76 (C) STRANDEDNESS: double
77 (D) TOPOLOGY: linear
78
79 (ii) MOLECULE TYPE: DNA (cdna)
80
81 (ix) FEATURE:
82 (A) NAME/KEY: CDS
83 (B) LOCATION: 169..1122
84
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
86
87 GGAGAGGGTG TGAGGGCAGA TCTGGGGGTG CCCAGATGGA AGGAGGCAGG CATGGGGGAC 60
88
89 ACCCAAGGCC CCCTGGCAGC ACCATGAACT AAGCAGGACA CCTGGAGGGG AAGAACTGTG 120
90
91 GGGACCTGGA GGCCTCCAAC GACTCCTTCC TGCTTCCTGG ACAGGACT ATG GCT GTG 177
92 Met Ala Val
93 1
94
95 CAG GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA 225
96 Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr
97 5 10 15
98
99 GCC ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC 273

RAW SEQUENCE LISTING PATENT APPLICATION US/10/052,545

DATE: 02/13/2002
TIME: 21:09:07

INPUT SET: S36758.raw

100	Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys	35
101	20 25 30	
102		
103	CTG GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG	321
104	Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val	
105	40 45 50	
106		
107	AGC TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG	369
108	Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg	
109	55 60 65	
110		
111	AAC CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG	417
112	Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser	
113	70 75 80	
114		
115	GAC CTG CTG GTG AGC GGG AGC AAC GTG CTG GAG ACG GCC GTC ATC CTC	465
116	Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala Val Ile Leu	
117	85 90 95	
118		
119	CTG CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG	513
120	Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln	
121	100 105 110 115	
122		
123	CTG GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC	561
124	Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser	
125	120 125 130	
126		
127	CTC TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC	609
128	Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe	
129	135 140 145	
130		
131	TAC GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CGG CGA	657
132	Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg Arg	
133	150 155 160	
134		
135	CGC GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC	705
136	Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe	
137	165 170 175	
138		
139	ATC GCC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC	753
140	Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe	
141	180 185 190 195	
142		
143	TTC CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG	801
144	Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu	
145	200 205 210	
146		
147	GCC CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG	849
148	Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg	
149	215 220 225	
150		
151	CAG CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC	897
152	Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu	

RAW SEQUENCE LISTING PATENT APPLICATION US/10/052,545

DATE: 02/13/2002
TIME: 21:09:07

INPUT SET: S36758.raw

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153          230          235          240
154
155 ACC ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG      945
156 Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu
157      245          250          255
158
159 CAT CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC      993
160 His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys
161 260          265          270          275
162
163 ATC TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC      1041
164 Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala
165      280          285          290
166
167 ATC ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG      1089
168 Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg
169      295          300          305
170
171 ACG CTC AAG GAG GTG CTG ACA TGC TCC TGG TGAGCGCGGT GCACGCGCTT      1139
172 Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
173      310          315
174
175 TAAGTGTGCT GGGCAGAGGG AGGTGGTGAT ATTGTGTGGT CTGGTTCCTG TGTGACCCTG      1199
176
177 GGCAGTTCCT TACCTCCCTG GTCCCCGTTT GTCAAAGAGG ATGGACTAAA TGATCTCTGA      1259
178
179 AAGTGTGAA G      1270
180
181
182 (2) INFORMATION FOR SEQ ID NO: 2:
183
184 (i) SEQUENCE CHARACTERISTICS:
185 (A) LENGTH: 317 amino acids
186 (B) TYPE: amino acid
187 (D) TOPOLOGY: linear
188
189 (ii) MOLECULE TYPE: polypeptide
190
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
192
193 Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
194 1          5          10          15
195
196 Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
197      20          25          30
198
199 Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
200      35          40          45
201
202 Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
203      50          55          60
204
205 Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu

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RAW SEQUENCE LISTING PATENT APPLICATION US/10/052,545

DATE: 02/13/2002
TIME: 21:09:08

INPUT SET: S36758.raw

	65	70	75	80
206				
207				
208	Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala			95
209		85	90	
210				
211	Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val		105	110
212		100		
213				
214	Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met		120	125
215		115		
216				
217	Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile		135	140
218		130		
219				
220	Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg		150	155
221		145		
222				
223	Ala Arg Arg Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser		165	170
224				175
225				
226	Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu		180	185
227				190
228				
229	Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val		195	200
230				205
231				
232	His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu		210	215
233				220
234				
235	His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala		225	230
236				235
237				
238	Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro		240	245
239		245		250
240				
241	Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr		255	260
242		260		265
243				270
244	Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile		275	280
245				285
246				
247	Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu		290	295
248				300
249				
250	Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp		305	310
251				315
252				
253				
254	(2) INFORMATION FOR SEQ ID NO: 3:			
255				
256	(i) SEQUENCE CHARACTERISTICS:			
257	(A) LENGTH: 33 base pairs			
258	(B) TYPE: nucleic acid			

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/10/052,545*DATE: 02/13/2002
TIME: 21:09:08*INPUT SET: S36758.raw*

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Jarl Wikberg
7	Unknown or Misplaced Identifier	(B) STREET: Trillvaegen 13
8	Unknown or Misplaced Identifier	(C) CITY: Umea
9	Unknown or Misplaced Identifier	(E) COUNTRY: Sweden
10	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 905 92 Umea
12	Unknown or Misplaced Identifier	(A) NAME: Vijay Chhajlani
13	Unknown or Misplaced Identifier	(B) STREET: Stigbergsvaegen
14	Unknown or Misplaced Identifier	(C) CITY: Uppsala
15	Unknown or Misplaced Identifier	(E) COUNTRY: Sweden
16	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 752 42 Uppsala

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/10/052,545*

DATE: 02/13/2002
TIME: 21:09:08

INPUT SET: S36758.raw

< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/10/052,545*

DATE: 02/13/2002
TIME: 21:09:08

INPUT SET: S36758.raw

Line	Original Text	Corrected Text
834	(xi) SEQUENCE DESCRIPTION: SEQ ID NO 17:	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17: